

OW of: US-09-652-292-2 to: EST:\* out\_format : pfs

Date: Mar 15, 2002 7:30 AM

About: Results were produced by the GenCore software, version 4.5,  
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Command-line parameters:

-MODE=framedat\_p2n.model -DRV=xlh  
-Q/cgna2/USPTO.spool/US09652292/runat\_13032002\_161725\_3195/app\_query.fasta\_1.606  
-DB-EST -QFMT=fastap -SUFFIX=est -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -CGAPOP=4.500  
-CGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -CGAPOP=6.000  
-CGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000  
-DELEXT=7.000 -START=1 -MATRIX=blossum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZ=500  
-MINLEN=0 -MAXLEN=200000000 -USER=US09652292 -CGN1\_1.4076  
-NCPU=6 -ICPU=3 -LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30  
-NO\_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-652-292-2  
Query length: 541  
Database: EST\*  
Database sequences: 11351937  
Database length: 1077921985  
Search time (sec): 1204.940000

score\_list:

Sequence	Strd	Orig	zScore	EScore	Len	Documentation ...
gb_est1.AL554162	+	1163.50	1484.02	1.7e-73	910	AL554162 AL554162 LTI_NFL006_PL2
gb_est1.AL449917	-	786.00	1007.12	6.2e-47	456	AL449914 AL449914 Homo sapiens
gb_est1.AL449887	+	781.00	1000.87	1.4e-46	459	AL449887 AL449887 Homo sapiens
gb_est1.AL449913	+	770.00	988.75	8.5e-46	461	AL449913 AL449913 Homo sapiens
gb_est1.AL449886	+	742.00	931.14	8.2e-44	450	AL449886 AL449886 Homo sapiens
gb_est1.BE237601	+	689.00	881.62	6.1e-40	540	BE237601 146953 MARC 4BOV Bos t
gb_est2.BF706879	+	623.00	791.00	6.8e-35	1049	BF706879 602184982F1 NIH_MGC_4
gb_est2.BF706976	+	553.00	708.65	2.6e-30	481	BF706976 281657 MARC 3BOV Bos t
gb_est1.AA313045	+	473.00	610.46	7.7e-25	306	AA313045 EST183920 Pancreas tum
gb_est1.AL449905	-	445.00	572.10	1.1e-22	402	AL449905 AL449905 Homo sapiens
gb_est2.BF615211	+	433.50	555.12	9.3e-22	513	BF615211 G082804.x1 Wellcome CH
gb_est2.BF612918	+	403.00	516.50	1.3e-19	491	BF612918 G078801.x2 Wellcome CH
gb_hcc.AK005068	+	403.00	501.27	9.3e-19	2538	AK005068 Mus musculus adult ma
gb_est1.AL449904	+	398.00	512.09	2.3e-19	396	AL449904 AL449904 Homo sapiens
gb_est1.AG14852	+	377.00	489.56	4.2e-18	248	AG14852 vF9508.y1 Soares_mam
gb_est1.AG14852	+	358.00	455.74	3.2e-16	691	AG14852 G078801.y1 Wellcome CH
gb_est2.BF611497	+	353.00	426.24	1.1e-15	966	BF611497 Tetraodon nigroviridis
gb_gss.CNS0498V	+	332.00	421.74	2.5e-14	747	BF789282 G02105191F1 NCI_CGAP_X
gb_est2.BF789282	+	332.00	412.60	8.1e-14	2003	AA115084 M0018 RCW Lambda Zap
gb_est1.AA415084	+	320.50	408.73	1.3e-13	622	AA118747 DRF2P76100210.rl 761
gb_est2.BF611325	-	315.50	401.15	3.5e-13	706	BF611325 G078801.y1 Wellcome CH
gb_est1.AV384186	+	311.00	395.41	7.3e-13	705	AV384186 AV384186 Halocynthia r
gb_est1.AW386065	+	303.50	386.27	2.4e-12	671	AW386065 EST317688 MHAM Medicag
gb_est1.BE641687	-	298.00	377.25	7.5e-12	831	BE641687 Cr12.3_P16_SP6 Ceratop
gb_est1.AL449468	-	294.00	384.66	2.9e-12	215	AL449468 AL449468 Homo sapiens
gb_est1.AL449471	-	293.00	382.64	3.8e-12	233	AL449471 AL449471 Homo sapiens
gb_est1.AL449916	-	291.00	381.00	4.7e-12	211	AL449916 AL449916 Homo sapiens
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gb_est1.AA461907	+	289.00	378.75	6.2e-12	204	AA461907 vF9508.y1 Soares_mam
gb_est2.BF328407	+	288.50	377.98	6.9e-12	207	BF328407 PM3-BN0174-230500-006
gb_est1.AW657233	+	285.00	364.45	3.9e-11	549	AW657233 109952 MARC 1BOV Bos t
gb_est1.AL449891	+	284.00	373.51	1.2e-11	180	AL449891 AL449891 Homo sapiens
gb_est1.AW561030	+	281.00	357.49	9.5e-11	670	AW561030 EST316078 DSIR Medicag
gb_est1.AV383222	+	280.50	355.85	1.2e-10	746	AV383222 AV383222 Halocynthia r
gb_est2.BF033803	+	279.50	353.65	1.6e-10	824	BF033803 G01454148F1 NIH_MGC_6
gb_est1.AW934681	-	275.50	349.88	2.5e-10	712	AW934681 EST335373 tomato flowe
gb_est1.AW940827	-	275.00	347.55	3.4e-10	855	AW940827 GH21490.3prime GH Dro
gb_gss.AQ989426	+	274.50	351.03	2.2e-10	548	AQ989426 Cm_UMB001.157_J16F UMN
gb_gss.CNS06VUO	-	273.00	343.53	5.7e-10	1000	AL417624 T7 end of clones AX0A
gb_est2.R59842	+	272.00	348.27	3.1e-10	523	R59842 yhl1908.rl Soares infan

gb\_gss.CNS06VME - 270.50 339.85 9.1e-10 1054 ! AL405660 T3 end of clone AU  
gb\_est1.AL449917 - 267.00 349.98 2.5e-10 218 ! AL449917 AL449917 Homo sapie  
gb\_est1.AL449467 - 264.00 347.61 3.4e-10 186 ! AL449467 AL449467 Homo sapie  
gb\_est2.BI268049 + 264.00 335.84 1.5e-09 662 ! BI268049 NF119G09IN1F1072 In  
gb\_est2.BE910478 + 262.50 330.73 2.9e-09 934 ! BE910478 601501005F1 NIH\_MGC  
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seq\_documentation\_block: 910 bp mRNA EST 16-FEB-2001  
LOCUS AL554162 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CS0D1081YA24 5  
DEFINITION AL554162 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CS0D1081YA24 5  
prime, mRNA sequence.  
ACCESSION AL554162  
VERSION AL554162.1 GI:12894675  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 910)  
AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
FEATURES  
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/clone="CS0D1081YA24"  
/tissue\_type="placenta"  
/note="vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with NotI and  
cloned into the NotI and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed by  
Life Technologies. Contact : Feng Liang Life Technologies,  
a division of Invitrogen 9800 Medical Center Drive  
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com

BASE COUNT 115 a 282 c 264 g 222 t 27 others  
ORIGIN  
alignment\_scores: Quality: 1163.50 Length: 281  
Ratio: 4.458 Gaps: 4  
Percent Similarity: 92.883 Percent Identity: 90.391  
alignment\_block:  
US-09-652-292-2 x AL554162 ..  
Align seg 1/1 to: AL554162 from: 1 to: 910  
1 MetGlyHisSerProValLeuProLeuCysAlaSerValSerLeuLe 17  
||||| ||| |||||||||||||||||||||||||||||||||||  
72 ATGGGGCACTTCACCTGTCGCTTGTGTGGCTCTGTGCTTGTGCT 121  
17 uGly...GlyLeuThrPheGlyTyrGluLeuAlaValIleSerGlyAlaL 33  
||||| |||||||||||||||||||||||||||||||||||  
122 GCGCTGTGGCTGACCTTTGGTTTATGACCTGGVGTATATCAGGTGCC 171  
33 euLeuProLeuGlnLeuAapphe.....GlyLeuSerCysLeuGluGln 47  
||||| |||||||||||||||||||||||||||||||  
172 TGTGCTGCACTGCAGCTGACTTTTGGCTTGTGGCTTGTGCTTGTGCT 221  
48 GluPheLeuValGlySerLeuLeuLeuGlyAlaLeuAlaSerLeuVa 64  
||||| ||| ||||||| |||  
222 TCCTKTKTKKGCAGCTGCTCTCTGGGGGTCCTCTCTCTCTCTCTCTCT 271



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VERSION AL449887.1 GI:11181512
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 459)
JOURNAL Stavrides,G.S., Huckle,E.J. and Deloukas,P.
COMMENT Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P
Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : sccd1338.
FEATURES
source
1..459
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_lib="Homo sapiens fetal lung (Stavrides GS)"
/tissue_type="Lung"
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/note="cDNA fragment isolated using a cDNA end rescue
technique"
BASE COUNT 74 a 148 c 142 g 95 t
ORIGIN

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Ratio: 5.105 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.346

alignment_block:
US-09-652-292-2 x AL449887
Align seg 1/1 to: AL449887 from: 1 to: 459
162 TrpGlyTrpArgHisMetPheGlyTrpAlaThrAlaProAlaValLeuGI 178
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1 TGGGGATGAGGCACATGTTGGCTGGGCCACTGCACCTGCTCTCTGCA 50
|||||
178 nSerLeuSerLeuLeuPheLeuProAlaGlyThrAspGluThrAlaThrH 195
|||||
51 ATCCCTCAGCCTCCTCTTCTCCTCTGCTGCTACAGATGAGACTGCAACAC 100
|||||
195 iSLysAspLeuIleProLeuGlnGlyGluAlaProLysLeuGlyPro 211
|||||
101 ACAAGGACCTCATCCACCTCCAGGGAGGTGAGGCCCCCAAGCTGGGCCG 150
|||||
212 GlyArgProArgTyrSerPheLeuAspLeuPheArgAlaAspAsnMe 228
|||||
151 GGGAGGCCACGGTACTCTTCTGGACCTCTTCAGGCGACGGCATAAACAT 200
|||||
228 tArgGlyArgThrThrValGlyLeuGlyLeuValLeuPheGlnGlnLeuT 245
|||||
201 GCGAGCCGCGACACAGTGGGGCTGGGGCTGGTCTCTTCCAGCAACTAA 250
|||||
245 hrGlyGlnProAsnValLeuCysTyrAlaSerThrIlePheSerVal 261
|||||
251 CAGGGCGGCCCAACAGTGTGTGTATGGCTCCACCATCTTCAGCTCCGTT 300
|||||
262 GlyPheHisGlyGlySerSerAlaValLeuAlaSerValGlyLeuGlyAl 278
|||||
301 GGTTCCTCATGGGGATCCTCAGCCGCTGCTGCTCTGTGGGGCTGGCCG 350
|||||
278 aValLysValAlaAlaThrLeuThrAlaMetGlyLeuValAspArgAlaG 295
|||||
351 AGTAGAGTGGCAGCTACCTCAGCCCATGGGGCTGGTGGGCGGTGCAG 400
|||||
295 lyArgArgAlaLeuLeuAlaGlyCysAlaLeuMetAlaLeuSerVal 311
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401 GCCGCAAGCCTCTGTGTAGCTGGCTGTGCCCTCATGGCCCTGTCCGTC 450
312 SerGlyIle 314
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451 ACTGGCATA 459
seq_name: gb_est1:AL449913
seq_documentation_block: 461 bp mRNA EST 15-NOV-2000
LOCUS AL449913 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,
DEFINITION AL449913 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,
mRNA sequence.
ACCESSION AL449913
VERSION AL449913.1 GI:11181538
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 461)
JOURNAL Stavrides,G.S., Huckle,E.J. and Deloukas,P.
COMMENT Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P
Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : sccd3334.
FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_lib="Homo sapiens fetal lung (Stavrides GS)"
/tissue_type="Lung"
/dev_stage="fetal"
/note="cDNA fragment isolated using a cDNA end rescue
technique"
BASE COUNT 56 a 146 c 145 g 114 t
ORIGIN

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Ratio: 5.033 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-652-292-2 x AL449913
Align seg 1/1 to: AL449913 from: 1 to: 461
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2 TCAGGTGCCCTGCTGCCACTGCAGCTTGACTTTGGGCTAAGCTGCTTGA 51
|||||
46 uGlnGluPheLeuValGlySerLeuLeuLeuGlyAlaLeuLeuAlaSerL 63
|||||
52 GCAGGAGTTCCTGGTGGCAGCCTGCTCTCTGGGGGCTCTCTCGCTCCC 101
|||||
63 euValGlyGlyPheLeuIleAspCysTyrGlyArgLysGlnAlaIleLeu 79
|||||
102 TGGTGGTGGCTTCTCTCATTTGACTGTCTATGGCAGGAGCAAGCACTCC 151
|||||
80 GlySerAsnLeuValLeuLeuAlaGlySerLeuThrLeuGlyLeuAlaGI 96
|||||
152 GGGAGCAACTTGGTGTCTGGCAGGACGCTGACCTGGCCCTGGCTGGTGG 201
|||||
96 ySerLeuAlaTrpLeuValLeuGlyArgAlaValAlaValGlyPheAlaIle 113
|||||
202 TTCCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTTT 251
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113 erLeuSerSerMetAlaCysCysIleTyrValSerGluLeuValGlyPro 129
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|||||
252 CCCTCTCTCCATGCTTGGCTATCTACGTCTCAGAGCTGGTGGGCCA 301
|||||
130 ArgGlnArgGlyValLeuValSerLeuTyrGluAlaGlyIleThrValG1 146
|||||
302 CGGCAGCGGGAGTCTGGTGGCTCTATGAGGAGGATCAGCGTGGG 351
|||||
146 ylleLeuLeuSerTyrAlaLeuAsnTyrAlaLeuAlaGlyThrProTpg 163
352 CATCTGCTCTCTATGCTCCCTCACTATGCACTGGCTGGTACCCCTGGG 401
|||||
163 lyTrpArgHisMetPheGlyTrpAlaThrAlaProAlaValLeuGlnSer 179
|||||
402 GATGAGGACATGTTGGCTGGGCCACTGCACCTGCTGCTCTGCAATCC 451
180 LeuSerLeu 182
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452 CTCAGCCTC 460

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seq\_name: gb\_est1:AL449886

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seq_documentation_block:
LOCUS AL449886 450 bp mRNA EST 15-NOV-2000
DEFINITION AL449886 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,
mRNA sequence.
ACCESSION AL449886
VERSION AL449886.1 GI:11181511
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 450)
Stavrides,G.S., Huckle,E.J. and Deloukas,P.
Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P
JOURNAL
COMMENT Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name: sccdl336.

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## FEATURES

source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="cDNA fragment isolated using a cDNA end rescue
technique"
BASE COUNT 75 a 148 c 133 g 94 t
ORIGIN

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## alignment\_scores:

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Quality: 742.00 Length: 145
Ratio: 5.189 Gaps: 0
Percent Similarity: 98.621 Percent Identity: 98.621

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## alignment\_block:

US-09-652-292-2 x AL449886 ..

Align seg 1/1 to: AL449886 from: 1 to: 450

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128 GlyProArgGlnArgGlyValLeuValSerLeuTyrGluAlaGlyIleTh 144
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16 GGAATTCGGCAGCGGGAGTCTGGTGTCTCTATGAGCAGGCATCAC 65
|||||
144 rValGlyIleLeuSerTyrAlaLeuAsnTyrAlaLeuAlaGlyThrP 161
|||||
66 CTGGGCATCTCTCTCTATGCGCCCTCAACTATGCATGGCTGTATGCC 115

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161 roTrpGlyTrpArgHisMetPheGlyTrpAlaThrAlaProAlaValLeu 177
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116 CCTGGGATGGAGGCACATGTTGGCTGGGCCACTGCACCTGCTGCTCTG 165
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178 GlnSerLeuSerLeuLeuPheLeuProAlaGlyThrAspGluThrAlaTh 194
|||||
166 CAATCCCTCAGCTCTCTTCTCCCTCCCTGGTACAGATGAGACTGCAAC 215
|||||
194 rHisLysAspLeuIleProLeuGlnGlyGluAlaProLysLeuGlyP 211
216 ACACAGGAGCTCATCCACTCCAGGAGGTGAGGCCCCCAAGCTGGGCC 265
|||||
211 roGlyArgProArgTyrSerPheLeuAspLeuPheArgAlaArgAspAsn 227
|||||
266 CGGGAGGCCACCGTACTCTCTTCTGGACCTCTTCAGGGCAGCGATAAC 315
|||||
228 MetArgGlyArgThrThrValGlyLeuGlyLeuValLeuPheGlnGlnLe 244
|||||
316 ATGGAGGCCGGACACACAGTGGGCTGGGCTGTGCTCTTCCAGCAACT 365
|||||
244 uThrGlyGlnProAsnValLeuCystTyrAlaSerThrIlePheSerSerV 261
|||||
366 AACAGGCGACGCCCAAGCTGTGTCTATGCTTTCACCATCTTTCAGCTCCG 415
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261 alGlyPheHisGlyGlySerSerAlaValLeuAla 272
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416 TTGCTTTCCATGGGGATCTCTCAGCGCTGCTGGCC 450

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seq\_name: gb\_est1:BE237601

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seq_documentation_block:
LOCUS BE237601 540 bp mRNA EST 25-APR-2001
DEFINITION 146953 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE237601
VERSION BE237601.1 GI:9022319
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos..
1 (bases 1 to 540)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Chor,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Perte,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.

```

```

Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCAGCTCAGCAGC
Plate: 48 row: p column: 4
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
1. .540
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/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

```

## FEATURES

source

57 a	189 c	176 q	118 t
------	-------	-------	-------

Email: cgapdgs-femail@nhi.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLOC1156 row: d column: 22

Location/Qualifiers  
1. .1049

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/organism="Homo sapiens"  
/db_xref="taxon:9606"
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/cclone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"

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NOTE: Organ, eye, vector, site\_1, xhoI, site\_2, EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Kuo (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library. 1"

231 a 331 c 429 g 458 c

cores:		
Quality:	623.00	Length: 122
Ratio:	5.107	Gaps: 0
Similarity:	100.000	Percent Identity: 99.180

LOCK : 92-2 x BF688799 . .

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/1 to: BF688799 from: 1 to: 1049
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IleTyrProValGluIleArgGlyArgAlaPheAlaPheCysAsnS 453

104  
 469

TCGAAC TGGGGGCCAACCTCTTCATCAGCCCTCTCCTTCGATCTC 154  
eglyThrIleGlyLeuSerTrp<sup>h</sup>PheLeuLeuTyrGlyLeuThrAl 486

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serLeuAlaGlnIleAspGlnGlnPheGlnIleValArgArgPheThrLeu 519  
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CGTTGGCAGAGATAGACCAGCAGT

**PROBATION DEPARTMENT**

eSerAlaIaSer 541  
 |||||  
 CTCTGGGGCTCC 370  
 TTTTGGCCACAGGCAGNACTCCACTGGCATCCCTACGCCGATCGA 354

seq\_name: gb\_est2:BF706976

seq\_documentation\_block: 481 bp mRNA EST 25-APR-2001  
 LOCUS BF706976 281657 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.  
 DEFINITION BF706976  
 ACCESSION BF706976  
 VERSION BF706976.1 GI:11998637  
 KEYWORDS EST.  
 SOURCE cow.

# ORGANISM

Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bos.

# REFERENCE

1 (bases 1 to 481)  
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,  
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,  
 G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,  
 Portea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and  
 Keele, J.W.  
 Sequence evaluation of four pooled-tissue normalized bovine cDNA  
 libraries and construction of a gene index for cattle  
 Genome Res. 11 (4), 626-630 (2001)  
 21180013

# TITLE

Genome Res. 11 (4), 626-630 (2001)

# JOURNAL

# MEDLINE

# COMMENT

Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@mail.marc.usda.gov  
 Single pass sequencing. Bases called and alt\_trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -minscore 18  
 and -mismatch 12 options.  
 PCR primers

FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCAGTCAGGAGC  
 Plate: 79 row: F column: 16  
 Seq primer: ATTTAGTGACACTATAG.

# FEATURES

Source  
 1..481  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="MARC 3BOV"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV SPORT6; Site1: XbaI; Site2: XhoI;  
 Library made from pooled tissue from marrow, alveolar  
 macrophage, ovary, fetal semitendinosus muscle, and fetal  
 longissimus muscle."  
 53 a 169 c 158 g 101 t  
 BASE COUNT  
 ORIGIN

# alignment\_scores:

Quality: 553.00 Length: 132  
 Ratio: 4.424 Gaps: 0  
 Percent similarity: 94.697 Percent identity: 87.121

# alignment\_block:

US-09-652-292-2 x BF706976 ..  
 Align seg 1/1 to: BF706976 from: 1 to: 481

1 MetGlyHisSerProValLeuProLeuCysAlaSerValSerLeuLe 17

86 ATGGCGCGACCTTCACCTCTCGCTGCTGAGAGCTCGGTGCTTCTGCT 135

17 uGlyGlyLeuThrPheGlyTyrGluLeuAlaValIleSerGlyAlaLeu 34

136 GGGTGGCCCTGAGCTTTGGCTATGAATGGCAGTCATATCGGGTGCCTCC 185

34 euProLeuGlnLeuAspPheGlyLeuSerCysLeuGluGlnGluPheLeu 50

186 TGGCGCTGACGCTTATTTTCGGGCTGAGCTGCTCAGCAGCAGGACTTCTG 235

51 ValGlySerLeuLeuLeuGlyAlaLeuLeuAlaSerLeuValGlyGlyph 67  
 236 GTGGCAGCTGCTCCTGGGGGCTCTCTCTGCTCCTCTGCTAGGGGCTG 285  
 67 eLeulleAspCysTyrGlyArgLysGlnAlaIleLeuGlySerAsnLeu 84  
 286 CCTCATCGACCGCTATGCGGGAAGCAGCATCTCGGGAGCAACTTGG 335  
 84 alLeuLeuAlaGlySerLeuThrLeuGlyLeuAlaGlySerLeuAlaTri 100  
 336 TGCTGTTGGCAGGAGCTGAGCTGGCGCTGGCGGCTCCCTGCGCTGG 385  
 101 LeuValLeuGlyArgAlaValValGlyPheAlaIleSerLeuSerSerMe 117  
 386 CTGCTCTGGCGCGCTCGGTGGGTGTTTGGCCATCTCCCTCTCCAT 435  
 117 tAlaCysCysIleTyrValSerGluLeuValGlyProArgGlnArg 132  
 436 GGCTGCTGCTCATCAGCTGTCGAGCTGGCGGCGCCACGCGCAGCG 481

seq\_name: gb\_est1:AA313045

seq\_documentation\_block:

LOCUS AA313045 306 bp mRNA EST 19-APR-1997  
 DEFINITION EST183920 Pancreas tumor I Homo sapiens cDNA 5' end similar to  
 similar to glucose transporter, mRNA sequence.  
 ACCESSION AA313045  
 VERSION AA313045.1 GI:1965446  
 KEYWORDS EST.  
 SOURCE human.

# ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

# REFERENCE

1 (bases 1 to 306)  
 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult,  
 C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White,  
 O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,  
 Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald,  
 L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,  
 Gnehm, C.L., Hanna, M.C., Hdbloom, E., Hinkle, P.S., Jr., Kelley, J.M.,  
 Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,  
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,  
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,  
 Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,  
 Begnarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,  
 Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,  
 Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,  
 Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L.,  
 Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon,  
 M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and  
 Venter, J.C.

Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl), 3-174 (1995)  
 96026280

# CONTACT:

Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org

For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/ldb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

Location/Qualifiers  
 1..306  
 /organism="Homo sapiens"  
 /db\_xref="ATCC (inhost):190186"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Pancreas tumor I"

# FEATURES

source

/dev\_stage="adult"  
 /note="Organ: pancreas; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"  
 BASE COUNT 61 a 95 c 73 t 5 others  
 ORIGIN

alignment\_scores:  
 Quality: 473.00 Length: 96  
 Ratio: 5.032 Caps: 0  
 Percent Similarity: 97.917 Percent Identity: 95.833

alignment\_block:  
 US-09-652-292-2 x AA313045

Align seg 1/1 to: AA313045 from: 1 to: 306

444 ATGGTGAAGGAGCTTCGCTTCTGCAACAGCTTCACTGGCGGCCAACCT 50  
 1 CGAGGAGAGGCTTCGCTTCTGCAACAGCTTCACTGGCGGCCAACCT 50  
 460 uPheileSerLeuSerPheLeuAspLeuileGlyThrileGlyLeuSerT 477  
 51 CTTATCATGCGCTCTCTCTGATCTCATTTGGCACCATCGGCTTGTCT 100  
 477 rPThrPheLeuLeuTyrGlyLeuThrAlaValLeuGlyLeuGlyPheile 493  
 101 GGACCTTCTGCTTACGAGACTGACGCTGTCTCGGCTGGGCTTCATC 150  
 494 TyrLeuPheValProGluThrLysGlyGlnSerLeuAlaGluileAspGI 510  
 151 TATTTATTTGTTCTTGAACAAAGGCCAGTCTGGCAGAGATAGACCA 200  
 510 nGlnPheGlnLysArgPheThrLeuSerPheGlyHISArgGlnAsnS 527  
 201 GCAGTTNCAGAGAGAGCGGTTTCACTGAGCTTNGCCAGAGCAGAACT 250  
 527 eThrGlyLeuProTyrSerArgIleGluileSerAla 539  
 251 CCACCTGGCATCCGTACAGCGCATCGAGATCTCTGCG 288

seq\_name: gb\_est1.AL449905

seq\_documentation\_block:  
 LOCUS AL449905 402 bp mRNA EST 15-NOV-2000  
 DEFINITION AL449905 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,  
 mRNA sequence.  
 ACCESSION AL449905  
 VERSION AL449905.1 GI:11181530  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Stavrides,G.S., Huckle,E.J. and Deloukas,P.  
 TITLE Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P.  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Stavrides GS  
 The Sanger Centre  
 Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK  
 Email: humquery@sanger.ac.uk  
 Sanger Centre name: scc3095.  
 Location/Qualifiers

FEATURES  
 source 1..402  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /map="20"  
 /clone\_lib="Homo sapiens fetal lung (Stavrides GS)"  
 /tissue\_type="lung"  
 /dev\_stage="fetal"  
 /note="cDNA fragment isolated using a cDNA end rescue technique"

BASE COUNT 99 a 97 c 129 g 77 t  
 ORIGIN  
 alignment\_scores:  
 Quality: 445.00 Length: 89  
 Ratio: 5.057 Gaps: 0  
 Percent Similarity: 98.876 Percent Identity: 98.876

alignment\_block:  
 US-09-652-292-2 x AL449905/rev

Align seg 1/1 to reverse of: AL449905 from: 1 to: 402

453 SerPheAsnTrpAlaAlaAsnLeuPheileSerLeuSerPheLeuAspLe 469  
 397 TCTTCAAACTGGCGGCCAACCTCTTCAATCAGCCTCTCCTTCCTCATG 348  
 469 uTleGlyThrileGlyLeuSerTrpThrPheLeuLeuTyrGlyLeuThra 486  
 347 CATTTGCACCATCGGCTTGTCTGGACCTTCTTCTACGGACTGACCG 298  
 486 laValLeuGlyLeuGlyPheileTyrLeuPheValProGluThrLysGly 502  
 297 CTGCTCTCGGCTGGGCTTCATCTATTATTGTTCTTCTGAAACAAAGGC 248  
 503 GlnSerLeuAlaGluileAspGlnGlnPheGlnLysArgPheThrLe 519  
 247 CAGTCTTGGCAGAGATAGACAGCAGTTCACAGAGACGAGGTTACACCT 198  
 519 uSerPheGlyHISArgGlnAsnSerThrGlyThrileProTyrSerArgIleG 536  
 197 GAGCTTGGCCACAGCAGAACTCCACTGGCATCCGCTACAGCCGATCG 148  
 536 luileSerAlaAlaSer 541  
 147 AGATCTCTCGGCTCTCC 131

seq\_name: gb\_est2:BF615211

seq\_documentation\_block:  
 LOCUS BF615211 513 bp mRNA EST 14-DEC-2000  
 DEFINITION dd82a04.x1 Wellcome CRC pcDNA1 egg Xenopus laevis cDNA clone  
 IMAGE:3430566 3' similar to TR:095528 095528 DH28H20.1 ; mRNA  
 sequence.  
 ACCESSION BF615211  
 VERSION BF615211.1 GI:11788593  
 KEYWORDS EST.  
 SOURCE African clawed frog.  
 ORGANISM Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 Xenopodinae; Xenopus.  
 REFERENCE 1 (bases 1 to 513)  
 AUTHORS Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,  
 Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person  
 ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,  
 Waterston,R. and Willson,R.  
 TITLE WashU Xenopus EST project, 1999  
 JOURNAL Unpublished (1999)  
 COMMENT Other\_ESTs: dd82a04.y1  
 Contact: Sandy Clifton, Ph.D.  
 WashU Xenopus EST project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Library constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.  
 Gurdon, (Wellcome/CRC Institute). DNA Sequencing by: Washington  
 University Genome Sequencing Center  
 Clone distribution: Xenopus clones from this library are available  
 through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 444.

## FEATURES

source  
1..513

/organism="Xenopus laevis"  
/db\_xref="taxon:8355"  
/clone="IMAGE:3430566"  
/tissue\_type="egg"  
/lab\_host="DH10B (phage-resistant)"  
/note="Vector: pCDNA1; Site\_1: NotI; Site\_2: EcoRI; cDNAs  
were oligo-dr primed and directionally cloned. Library was  
constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.  
Gurdon (Wellcome/CRC Institute)."

BASE COUNT 138 a 113 c 122 g 140 t

## ORIGIN

alignment\_scores:  
Quality: 433.50 Length: 169  
Ratio: 3.583 Gaps: 2  
Percent Similarity: 71.598 Percent Identity: 52.071

## alignment\_block:

US-09-652-292-2 x BF615211

Align seg 1/1 to: BF615211 from: 1 to: 513

405 HisAlaLeuLeuArgTrpThrAlaLeuLeuCysLeuMetValPheVal 421  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
8 TATGCCATTTTGAACGTGATGAATCTTGTGAGCATGATGGCTTTGTAG 57

421 rAlaPheSerPheGlyPheGlyProValThrTrpLeuValLeuSerGluI 438

58 TGCCTTTTCCATTCGATTTGCTCAATGACCTGGTGTAGTGTGAGTCAA 107

438 LeuTyrProValGluLeuArgGlyArgAlaPheAlaPheCysAsnSerPhe 454

108 TCTATCCAGCGGACATCAGAGGAGACATTTGCTTCTCAACAGCTTC 157

455 AsnTrpAlaAlaAsnLeuPheLeuSerPheLeuAspLeuLeuLeI 471

158 AACTGGGCTGCCAATCTGCTTACTTACTTACCTTATTTGCAAGTTATGG 207

471 yThrIleGlyLeuSerTrpThrPheLeuLeuTyrGlyLeuThrAlaVal 488

208 TTCTATAGGCTGGCGTGGACTTTTGTCTAGCTAGGCTGGGCTGTC 257

488 euGlyLeuGlyPheIleTyrLeuPheValProGluThrLysGlyGlnSer 504

258 TGGCATTGGCTTCACTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 307

505 LeuAlaGluLeuAspGlnGlnPhe.Gln..... 513

308 CTCGAAGAATCGATCAACAGTTGTCAGCGAAGTTCGCTTAAAGCAGC 357

513 ..... 513

358 TAACCAAGAGTGTGCGGCAATGAGAGCGTTTCCGCCAGCGCTCAG 407

514 .....LysArgArgPhe 517

408 GAAACAGCACATGCAATAACATGTTTATCAAGGATATCAAGAGAGAGA 457

517 ePrlLeuSerPheGlyHisArgGlnAsnSerThrGlyIleProTyrSera 534

458 ACATCTAAAGCGGTTCGAAGAGACCATCCACTGCCCTCCATACACAA 507

534 rgile 535

508 GAGTA 512

seq\_name: gb\_est2:BF612918

seq\_documentation\_block:

LOCUS BF612918 491 bp mRNA EST 14-DEC-2000  
DEFINITION dd78h01.x2 Wellcome CRC pCDNA1 egg Xenopus laevis cDNA clone  
IMAGE:3430512 3' similar to TR:095528 095528 DH28H20.1 ; mRNA  
sequence.

ACCESSION BF612918 1 GF:11784031

VERSION BF612918

KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM

Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 491)

AUTHORS Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,  
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,  
B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,  
Waterston,R. and Wilson,R.

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Other ESTs: dd78h01.y1

Contact: Sandy Clifton, Ph.D.

WashU Xenopus EST project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Library constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.

Gurdon, (Wellcome/CRC Institute). DNA Sequencing by: Washington

University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available

through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

Possible reversed clone: similarity on wrong strand

Seq primer: -40UP from Gibco

High quality sequence stop: 452.

FEATURES

Location/Qualifiers

1..491

/organism="Xenopus laevis"

/db\_xref="taxon:8355"

/clone="IMAGE:3430512"

/clone\_lib="Wellcome CRC pCDNA1 egg"

/tissue\_type="egg"

/lab\_host="DH10B (phage-resistant)"

/note="Vector: pCDNA1; Site\_1: NotI; Site\_2: EcoRI; cDNAs

were oligo-dr primed and directionally cloned. Library was

constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.

Gurdon (Wellcome/CRC Institute)."

BASE COUNT 131 a 107 c 116 g 136 t 1 others

ORIGIN

alignment\_scores:

Quality: 403.00 Length: 111

Ratio: 3.838 Gaps: 0

Percent Similarity: 94.595 Percent Identity: 69.369

alignment\_block:

US-09-652-292-2 x BF612918

Align seg 1/1 to: BF612918 from: 1 to: 491

405 HisAlaLeuLeuArgTrpThrAlaLeuLeuCysLeuMetValPheVal 421

:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

8 TATGCCATTTTGAACGTGATGAATCTTGTGAGCATGATGGCTTTGTAG 57

421 rAlaPheSerPheGlyPheGlyProValThrTrpLeuValLeuSerGluI 438

|||||:::|||||:::|||||:::|||||:::|||||:::|||||

58 TGCCTTTTCCATTCGATTTGCTCAATGACCTGGTGTAGTGTGAGTCAA 107

438 LeuTyrProValGluLeuArgGlyArgAlaPheAlaPheCysAsnSerPhe 454





```

164 GCTGTACTAGTTCCTCCAGTTCGGCTATGACATCGGTGTGATCAATGC 213
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
31 yAla.....LeuLeuProLeuGlnL 38
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
214 ACCTCAAGAGGTAATANTCCATATCGACATGTTTGGGTGTTCAC 263
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
38 euAspPheGlyLeuSerCysLeu..... 45
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
264 TGGATGACCGGAAGTGCATTAACTATGAGTCAATGGGCACACACACC 313
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
46 .....GluG 47
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
314 CCACATTACAGTCACACAGCAGCATAACACACACAGCTCCCTGGGATGAAGA 363
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
47 nGlu.....PheLeu 51
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
364 GGAGACTGAAGCATCTGCTCACATAGTCACTATGCTCTGGTCTCTGTCTG 413
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
51 aIGlySerLeuLeuGlyAlaLeuAlaSerLeuValcIlyGlyPhe 67
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
414 TGTCCAGCTTTGCAGTGGGGGGAATGGTGGCTCATTTTGGTGGGTGG 463
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
68 LeuLeuAspCysTyrGlyArgIysGlnAlaIleLeuGlySerAsnLeuVa 84
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
464 CTCGGGGACAAACTTGAAGAGGATCAACAGCAATGTGGCTGCAAAACGCCT 513
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
84 lLeuLeuAlaGlySerLeuThrLeuGly.....LeuAlaGlySerL 98
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
514 CTCATTGACTGGAGCCCTCTGTATGGGATGTTCCAAATTTGGACCGGCAC 563
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
98 euAlaTrpLeuValLeuGlyArgAlaValValGlyPheAlaIleSerLeu 114
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
564 ACGCCCTCATCTTCTGGGAGGAGTGTATCAGGACTGTATTGGGCTA 613
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
115 SerSerMetAlaCysCysIleTyrValSerGluLeuValGlyProAlaG 131
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
614 ATTTACAGACTGGTTCCAAATGTATACATGGAGAGATCGCTCCACACACT 663
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
131 nArgGlyValLeuValSerLeuTyrGluAlaGlyIleThrValcIlyIleL 148
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
564 CAGGGTGGCCCTGGTACTCTTCCACCAACTGGCCCTTGTCCACAGGCATTC 713
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
148 euLeuSerTyr.....AlaLeuAsnTyrAlaLeuAlaGlyThrProTrp 162
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
714 TTATTAGTCAGATTGCTGGCCTCAGCTTTATTCTG...GGCAATCAGGAT 760
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
163 GlyTrpArgHisMetPheGlyTrpAlaThrAlaProAlaValLeuGlnSe 179
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
761 CATTTGGCACATCTACTTGGCCTATCTGCTGTGCCAGCTCTTCTGCAGTG 810
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
179 rLeuSerLeuLeuPheLeuProAlaGly..... 188
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
811 TCTGCTACTCTCTTGTCCAGAAAGCCCCAGATACCTTTATATAAAGT 860
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
189 ..ThrAspGluThrAlaThrHisLysAspLeuIleProLeuGlnGlyGly 204
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
861 TCGAAGAGGAAGTCAGGCAAGAAAGCTTGAAGAGACTAGAGGAAC 910
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
205 Glu.....AlaProLysLeuG 210
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
911 GAGGATGTCACCAAGATATTATGAGATGAAGAAAGAAAGAGAGGC 960
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
210 yProGlyArgProArgTyrSerPheLeuAspLeuPheArgAlaArgAspA 227
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
961 ATCGACTGAGCAGAGCTCTCGTGATCCAGCTCTTC...ACGGATGCCA 1007
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
227 snMetArgGlyArgThrThrValGlyLeuGlyLeuValLeuPheGlnGln 243
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
1008 ATTACCGACAGGCCCATCTCTGCTGGCGCTGATCTGCACATGCCCCAGCAG 1057
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
244 LeuThrGlyGlnProAsnValLeuLeuCysTyrAlaSerThrIlePheSerSe 260
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::

```

```

1058 TTCTCAGGAATCAATGGGATATTTTACTATTTCACACAGCAATTTTCAGAC 1107
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
260 rValcGlyPheHisGlyGlySerSerAlaValLeuAlaSerValGlyLeuG 277
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
1108 AGCTGGGCATC.....AGCCAGCCTGTGTATGCAACCACTTGTGTGG 1148
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
277 lYAlaValLysValAlaAlaThrLeuThrAlaMetGlyLeuValAspArg 293
      :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
1149 GGGGCATCAACATGATCTTCACGCTGTCTGTGCTGCTTGTGGAGAAG 1198
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294 AlaGlyArgArgAlaLeuLeuAlaGlyCysAlaLeuMetAlaLeuSe 310
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1199 GCAGGGCGGGGACCCTGTTCCTTACCAGGATG..... 1231
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310 rValSerGlyIleGlyLeuValSerPheAlaValProMetAspSerGlyP 327
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1232 .....ATTGGCATGTTTTTCTGCACCATCTTCATCTCGTGGGAC 1271
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327 rOSerCysLeuAlaValProAsnAlaThrGlyGlnThrGlyLeuProGly 343
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1272 TT..... 1273
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1288 ..... 1288
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1288 ..... 1288
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394 AlaLeuProGlyProProLeuProAlaArgGlyHisAlaLeuLeuArgTr 410
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1289 .....TTGCGCCTGGATGAGTTA 1305
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427 heGlyProValThrTrpLeuValLeuSerGluIleTyrProValGluIle 443
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494 TyrLeuPheValProGluThrLysGlyGlnSerLeuAlaGluIleAspG 510
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1553 TCTTTAAAGTTCCAGAAACCAAGAAAGTCTTTTGAGGAATCGCTGC 1602
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510 nGlnPheGlnLysArg 515
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DEFINITION AL449904 Homo sapiens mRNA sequence.
ACCESSION AL449904

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VERSION AL449904.1 GI:11181529
KEYWORDS EST.
SOURCE human.
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 396)
JOURNAL Stavrides,G.S., Huckle,E.J. and Deloukas,P.
COMMENT Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P
Unpublished (2000)
Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : sccg3094.
FEATURES
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BASE COUNT 77 a 122 c 99 g 97 t 1 others
ORIGIN

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2 AGCCTCTCTCTCGATCATCTGGCAGCATCGGCTTGCTGGACCTT 51
479 eLeuLeuTyrrGlyLeuThrAlaValLeuGlyLeuGlyPheIleTyrrLeuP 496
52 CCTGCTCTACGAGCTACCGCTGCTCGCGCTTGGCTTCATCTATTAT 101
496 heValProGluThrLysGlyGlnSerLeuAlaGluIleAspGlnPhe 512
102 TTGTTCTCAACAAAGGCCAGCTGTTGGCAGAGATAGACCAGCATGTC 151
513 GlnLysArgArgPheThrLeuSerPheGlyHisArgGlnAsnSerThrGI 529
152 CAGACAGACGGTTACCTCCCTGAGCTTTGGCCACAGCAGACCTCCACTG 201
529 yIleProTyrrSerArgIleGluIleSerAlaAlaSer 541
202 CATCCCGTACAGCCGATCGAGATCTCTCGGCCCTCC 238
seq_name: gb_est1:AI614852
seq_documentation_block:
LOCUS AI614852 248 bp mRNA EST 21-APR-1999
DEFINITION vF95908.y1 Soares_mammary_gland_MBMG Mus musculus cDNA clone
IMAGE:851582 5' similar to TR:032289 O32289 YXCC PROTEIN. ;, mRNA
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VERSION AI614852.1 GI:4624019
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SOURCE house mouse.
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 248)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:503734
This read is a RESEQUENCE of a previously sequenced mouse clone
correct orientation).
Seq primer: -40RP from Glibco
High quality sequence stop: 243.
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        primer [5'
        TGTACCAATCTGAATGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTT
        T 3']; double-stranded cDNA was ligated to Eco RI
        adaptors (Pharmacia), digested with Not I and cloned into
        the Not I and Eco RI sites of the modified pT7T3 vector.
        RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
        constructed and normalized by Bento Soares and M.Patina
        Bonaldo."
BASE COUNT 48 a 76 c 57 g 57 t
ORIGIN

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460 uPheIleSerLeuSerPheLeuAspLeuIleGlyThrIleGlyLeuSerT 477
52 CTTTATCAGCCTCTCCTTCCTCGACCTGATCGGTGCGCTTGGCTT 101
477 rpThrPheLeuLeuTyrrGlyLeuThrAlaValLeuGlyLeuGlyPheIle 493
102 GGACCTTCCTGCTCTAAGGCTGACCGCTGCTCTGGCTTGGCTTTCATC 151
494 TyrLeuPheValProGluThrLysGlyGlnSerLeuAlaGluIleAspGI 510
152 TACCTACTTGTCTCTCAACCAAGGACAGCTCTTTAGCTGAATAGACGA 201
510 nGlnPheGlnLysArgArgPheThrLeuSerPheGlyHisArgGln 525
202 GCAGTTTCAGCAAGCAGGCTTCCTCTAAACTTTGGCCATAGGCAG 247

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